

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Soderlund, David M.
Knipple, Douglas C.
Ingles, Patricia J.

(ii) TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT
HOUSE FLIES

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
(B) STREET: P.O. Box 1051, Clinton Square
(C) CITY: Rochester
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 14603

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/608,618
(B) FILING DATE: 01-MAR-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Braman, Susan J.
(B) REGISTRATION NUMBER: 34,103
(C) REFERENCE/DOCKET NUMBER: 19603/601 (CRF D-1657)

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 716-263-1636
(B) TELEFAX: 716-263-1600

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

09428371-102899

(A) LENGTH: 6318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGCTTCCCGC CGGAATTGGC CTCCACTCCT CTCGAGGATA TCGATCCCTT CTACAGTAAT	300
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662207.428469

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CCGATCTTGG	CCGGCGACGA	GGAATCGCCG	TTCTGGCAAG	GATGGGGCAA	TTTACGACTG	3840
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GATATACTGT	ACTACATGGA	CAGGATATTT	ACGGTGATAT	TCTTTTTTGA	GATGTTGATC	4020
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CTCCGTGTGG TGAGAGTGGC CAAAGTGGGT CGTGTCCTGC GTTTAGTCAA GGGTGCCAAG 5160
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGACAGAAG ATTCCGACTC GATATCTGAG GAAGAACGCA GTTTGTTCCTG TCCCTTCACC 60
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GGTCCACAGC CGGATCCCAC ACTTGAACAG GGTGTGCCTA TACCTGTTCG AATGCAGGGC 240
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GTACTGACAT TTGTAGTAAT AAGTAAAGGA AAGGATATTT TTCGTTTTTC TGCCTCAAAA 360
GCAATGTGGC TGCTCGATCC ATTCAATCCG ATACGTCGTG TAGCCATTTA TATTTTAGTG 420
CATCCCTTGT TTTCGTTATT CATTATCACC ACTATTCTAA CTAATTGTAT TTTAATGATA 480
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GGTACCCAGT	ACATAAGATA	CGACCAGCTG	TCCGAGTTCC	TGGACGTGCT	GGAGCCGCCG	5700
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ACGGCAGATG TCTGA 6315

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Thr	Glu	Asp	Ser	Asp	Ser	Ile	Ser	Glu	Glu	Glu	Arg	Ser	Leu	Phe
1				5				10						15	
Arg	Pro	Phe	Thr	Arg	Glu	Ser	Leu	Leu	Gln	Ile	Glu	Gln	Arg	Ile	Ala
			20				25						30		
Glu	His	Glu	Lys	Gln	Lys	Glu	Leu	Glu	Arg	Lys	Arg	Ala	Ala	Glu	Gly
		35				40					45				
Glu	Gln	Ile	Arg	Tyr	Asp	Asp	Glu	Asp	Glu	Asp	Glu	Gly	Pro	Gln	Pro
50					55				60						
Asp	Pro	Thr	Leu	Glu	Gln	Gly	Val	Pro	Ile	Pro	Val	Arg	Met	Gln	Gly
65					70				75					80	
Ser	Phe	Pro	Pro	Glu	Leu	Ala	Ser	Thr	Pro	Leu	Glu	Asp	Ile	Asp	Pro
				85					90					95	

Phe	Tyr	Ser	Asn	Val	Leu	Thr	Phe	Val	Val	Ile	Ser	Lys	Gly	Lys	Asp
			100					105					110		
Ile	Phe	Arg	Phe	Ser	Ala	Ser	Lys	Ala	Met	Trp	Leu	Leu	Asp	Pro	Phe
		115					120					125			
Asn	Pro	Ile	Arg	Arg	Val	Ala	Ile	Tyr	Ile	Leu	Val	His	Pro	Leu	Phe
	130					135					140				
Ser	Leu	Phe	Ile	Ile	Thr	Thr	Ile	Leu	Thr	Asn	Cys	Ile	Leu	Met	Ile
145					150					155					160
Met	Pro	Thr	Thr	Pro	Thr	Val	Glu	Ser	Thr	Glu	Val	Ile	Phe	Thr	Gly
				165					170					175	
Ile	Tyr	Thr	Phe	Glu	Ser	Ala	Val	Lys	Val	Met	Ala	Arg	Gly	Phe	Ile
			180					185					190		
Leu	Cys	Pro	Phe	Thr	Tyr	Leu	Arg	Asp	Ala	Trp	Asn	Trp	Leu	Asp	Phe
		195					200					205			
Val	Val	Ile	Ala	Leu	Ala	Tyr	Val	Thr	Met	Gly	Ile	Asp	Leu	Gly	Asn
	210					215					220				
Leu	Ala	Ala	Leu	Arg	Thr	Phe	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val
225					230					235					240
Ala	Ile	Val	Pro	Gly	Leu	Lys	Thr	Ile	Val	Gly	Ala	Val	Ile	Glu	Ser
				245					250					255	
Val	Lys	Asn	Leu	Arg	Asp	Val	Ile	Ile	Leu	Thr	Met	Phe	Ser	Leu	Ser
			260					265					270		
Val	Phe	Ala	Leu	Met	Gly	Leu	Gln	Ile	Tyr	Met	Gly	Val	Leu	Thr	Gln
		275					280					285			
Lys	Cys	Ile	Lys	Arg	Phe	Pro	Leu	Asp	Gly	Ser	Trp	Gly	Asn	Leu	Thr
	290					295					300				
Asp	Glu	Asn	Trp	Phe	Leu	His	Asn	Ser	Asn	Ser	Ser	Asn	Trp	Phe	Thr
305					310					315					320
Glu	Asn	Asp	Gly	Glu	Ser	Tyr	Pro	Val	Cys	Gly	Asn	Val	Ser	Gly	Ala
				325					330					335	
Gly	Gln	Cys	Gly	Glu	Asp	Tyr	Val	Cys	Leu	Gln	Gly	Phe	Gly	Pro	Asn
			340					345					350		

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Pro	Asn	Tyr	Asp	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Gly	Trp	Ala	Phe	Leu		
		355					360					365					
Ser	Ala	Phe	Arg	Leu	Met	Thr	Gln	Asp	Phe	Trp	Glu	Asp	Leu	Tyr	Gln		
	370					375					380						
His	Val	Leu	Gln	Ala	Ala	Gly	Pro	Trp	His	Met	Leu	Phe	Phe	Ile	Val		
385					390					395					400		
Ile	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	Ile		
				405					410					415			
Val	Ala	Met	Ser	Tyr	Asp	Glu	Leu	Gln	Lys	Lys	Ala	Glu	Glu	Glu	Glu		
			420					425					430				
Ala	Ala	Glu	Glu	Glu	Ala	Ile	Arg	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Ala		
		435					440					445					
Lys	Ala	Ala	Lys	Leu	Glu	Glu	Arg	Ala	Asn	Val	Ala	Ala	Gln	Ala	Ala		
	450					455					460						
Gln	Asp	Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ala	Leu	His	Pro	Glu	Met	Ala		
465					470					475					480		
Lys	Ser	Pro	Thr	Tyr	Ser	Cys	Ile	Ser	Tyr	Glu	Leu	Phe	Val	Gly	Gly		
				485					490					495			
Glu	Lys	Gly	Asn	Asp	Asp	Asn	Asn	Lys	Glu	Lys	Met	Ser	Ile	Arg	Ser		
			500					505					510				
Val	Glu	Val	Glu	Ser	Glu	Ser	Val	Ser	Val	Ile	Gln	Arg	Gln	Pro	Ala		
		515					520					525					
Pro	Thr	Thr	Ala	Pro	Ala	Thr	Lys	Val	Arg	Lys	Val	Ser	Thr	Thr	Ser		
	530					535					540						
Leu	Ser	Leu	Pro	Gly	Ser	Pro	Phe	Asn	Leu	Arg	Arg	Gly	Ser	Arg	Ser		
545					550					555					560		
Ser	His	Lys	Tyr	Thr	Ile	Arg	Asn	Gly	Arg	Gly	Arg	Phe	Gly	Ile	Pro		
				565					570					575			
Gly	Ser	Asp	Arg	Lys	Pro	Leu	Val	Leu	Gln	Thr	Tyr	Gln	Asp	Ala	Gln		
			580					585					590				
Gln	His	Leu	Pro	Tyr	Ala	Asp	Asp	Ser	Asn	Ala	Val	Thr	Pro	Met	Ser		
		595					600					605					

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Glu Glu Asn Gly Ala Ile Ile Val Pro Ala Tyr Tyr Cys Asn Leu Gly
610 615 620

Ser Arg His Ser Ser Tyr Thr Ser His Gln Ser Arg Ile Ser Tyr Thr
625 630 635 640

Ser His Gly Asp Leu Leu Gly Gly Met Ala Ala Met Gly Ala Ser Thr
645 650 655

Met Thr Lys Glu Ser Lys Leu Arg Ser Arg Asn Thr Arg Asn Gln Ser
660 665 670

Ile Gly Ala Ala Thr Asn Gly Gly Ser Ser Thr Ala Gly Gly Gly Tyr
675 680 685

Pro Asp Ala Asn His Lys Glu Gln Arg Asp Tyr Glu Met Gly Gln Asp
690 695 700

Tyr Thr Asp Glu Ala Gly Lys Ile Lys His His Asp Asn Pro Phe Ile
705 710 715 720

Glu Pro Val Gln Thr Gln Thr Val Val Asp Met Lys Asp Val Met Val
725 730 735

Leu Asn Asp Ile Ile Glu Gln Ala Ala Gly Arg His Ser Arg Ala Ser
740 745 750

Glu Arg Gly Glu Asp Asp Asp Glu Asp Gly Pro Thr Phe Lys Asp Ile
755 760 765

Ala Leu Glu Tyr Ile Leu Lys Gly Ile Glu Ile Phe Cys Val Trp Asp
770 775 780

Cys Cys Trp Val Trp Leu Lys Phe Gln Glu Trp Val Ser Phe Ile Val
785 790 795 800

Phe Asp Pro Phe Val Glu Leu Phe Ile Thr Leu Cys Ile Val Val Asn
805 810 815

Thr Met Phe Met Ala Met Asp His His Asp Met Asn Pro Glu Leu Glu
820 825 830

Lys Val Leu Lys Ser Gly Asn Tyr Phe Phe Thr Ala Thr Phe Ala Ile
835 840 845

Glu Ala Ser Met Lys Leu Met Ala Met Ser Pro Lys Tyr Tyr Phe Gln
850 855 860

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Glu	Gly	Trp	Asn	Ile	Phe	Asp	Phe	Ile	Ile	Val	Ala	Leu	Ser	Leu	Leu	865	870	875	880
Glu	Leu	Gly	Leu	Glu	Gly	Val	Gln	Gly	Leu	Ser	Val	Leu	Arg	Ser	Phe	885	890	895	
Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	900	905	910	
Leu	Leu	Ile	Ser	Ile	Met	Gly	Arg	Thr	Met	Gly	Ala	Leu	Gly	Asn	Leu	915	920	925	
Thr	Phe	Val	Leu	Cys	Ile	Ile	Ile	Phe	Ile	Phe	Ala	Val	Met	Gly	Met	930	935	940	
Gln	Leu	Phe	Gly	Lys	Asn	Tyr	Ile	Asp	His	Lys	Asp	Arg	Phe	Lys	Asp	945	950	955	960
His	Glu	Leu	Pro	Arg	Trp	Asn	Phe	Thr	Asp	Phe	Met	His	Ser	Phe	Met	965	970	975	
Ile	Val	Phe	Arg	Val	Leu	Cys	Gly	Glu	Trp	Ile	Glu	Ser	Met	Trp	Asp	980	985	990	
Cys	Met	Tyr	Val	Gly	Asp	Val	Ser	Cys	Ile	Pro	Phe	Phe	Leu	Ala	Thr	995	1000	1005	
Val	Val	Ile	Gly	Asn	Leu	Val	Val	Leu	Asn	Leu	Phe	Leu	Ala	Leu	Leu	1010	1015	1020	
Leu	Ser	Asn	Phe	Gly	Ser	Ser	Ser	Leu	Ser	Ala	Pro	Thr	Ala	Asp	Asn	1025	1030	1035	1040
Asp	Thr	Asn	Lys	Ile	Ala	Glu	Ala	Phe	Asn	Arg	Ile	Ala	Arg	Phe	Lys	1045	1050	1055	
Asn	Trp	Val	Lys	Arg	Asn	Ile	Ala	Asp	Cys	Phe	Lys	Leu	Ile	Arg	Asn	1060	1065	1070	
Lys	Leu	Thr	Asn	Gln	Ile	Ser	Asp	Gln	Pro	Ser	Glu	His	Gly	Asp	Asn	1075	1080	1085	
Glu	Leu	Glu	Leu	Gly	His	Asp	Glu	Ile	Met	Gly	Asp	Gly	Leu	Ile	Lys	1090	1095	1100	
Lys	Gly	Met	Lys	Gly	Glu	Thr	Gln	Leu	Glu	Val	Ala	Ile	Gly	Asp	Gly	1105	1110	1115	1120

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Met Glu Phe Thr Ile His Gly Asp Met Lys Asn Asn Lys Pro Lys Lys
1125 1130 1135

Ser Lys Phe Met Asn Asn Thr Thr Met Ile Gly Asn Ser Ile Asn His
1140 1145 1150

Gln Asp Asn Arg Leu Glu His Glu Leu Asn His Arg Gly Leu Ser Ile
1155 1160 1165

Gln Asp Asp Asp Thr Ala Ser Ile Asn Ser Tyr Gly Ser His Lys Asn
1170 1175 1180

Arg Pro Phe Lys Asp Glu Ser His Lys Gly Ser Ala Glu Thr Ile Glu
1185 1190 1195 1200

Gly Glu Glu Lys Arg Asp Val Ser Lys Glu Asp Leu Gly Leu Asp Glu
1205 1210 1215

Glu Leu Asp Glu Glu Ala Glu Gly Asp Glu Gly Gln Leu Asp Gly Asp
1220 1225 1230

Ile Ile Ile His Ala Gln Asn Asp Asp Glu Ile Ile Asp Asp Tyr Pro
1235 1240 1245

Ala Asp Cys Phe Pro Asp Ser Tyr Tyr Lys Lys Phe Pro Ile Leu Ala
1250 1255 1260

Gly Asp Glu Asp Ser Pro Phe Trp Gln Gly Trp Gly Asn Leu Arg Leu
1265 1270 1275 1280

Lys Thr Phe Gln Leu Ile Glu Asn Lys Tyr Phe Glu Thr Ala Val Ile
1285 1290 1295

Thr Met Ile Leu Met Ser Ser Leu Ala Leu Ala Leu Glu Asp Val His
1300 1305 1310

Leu Pro Asp Arg Pro Val Met Gln Asp Ile Leu Tyr Tyr Met Asp Arg
1315 1320 1325

Ile Phe Thr Val Ile Phe Phe Leu Glu Met Leu Ile Lys Trp Leu Ala
1330 1335 1340

Leu Gly Phe Lys Val Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe
1345 1350 1355 1360

Val Ile Val Met Leu Ser Leu Ile Asn Leu Val Ala Val Trp Ser Gly
1365 1370 1375

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Leu Asn Asp Ile Ala Val Phe Arg Ser Met Arg Thr Leu Arg Ala Leu
1380 1385 1390

Arg Pro Leu Arg Ala Val Ser Arg Trp Glu Gly Met Lys Val Val Val
1395 1400 1405

Asn Ala Leu Val Gln Ala Ile Pro Ser Ile Phe Asn Val Leu Leu Val
1410 1415 1420

Cys Leu Ile Phe Trp Leu Ile Phe Ala Ile Met Gly Val Gln Leu Phe
1425 1430 1435 1440

Ala Gly Lys Tyr Phe Lys Cys Lys Asp Gly Asn Asp Thr Val Leu Ser
1445 1450 1455

His Glu Ile Ile Pro Asn Arg Asn Ala Cys Lys Ser Glu Asn Tyr Thr
1460 1465 1470

Trp Glu Asn Ser Ala Met Asn Phe Asp His Val Gly Asn Ala Tyr Leu
1475 1480 1485

Cys Leu Phe Gln Val Ala Thr Phe Lys Gly Trp Ile Gln Ile Met Asn
1490 1495 1500

Asp Ala Ile Asp Ser Arg Glu Val Asp Lys Gln Pro Ile Arg Glu Thr
1505 1510 1515 1520

Asn Ile Tyr Met Tyr Leu Tyr Phe Val Phe Phe Ile Ile Phe Gly Ser
1525 1530 1535

Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn
1540 1545 1550

Glu Gln Lys Lys Lys Ala Gly Gly Ser Leu Glu Met Phe Met Thr Glu
1555 1560 1565

Asp Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Met Gly Ser Lys Lys
1570 1575 1580

Pro Leu Lys Ala Ile Pro Arg Pro Arg Trp Arg Pro Gln Ala Ile Val
1585 1590 1595 1600

Phe Glu Ile Val Thr Asp Lys Lys Phe Asp Ile Ile Ile Met Leu Phe
1605 1610 1615

Ile Gly Leu Asn Met Phe Thr Met Thr Leu Asp Arg Tyr Asp Ala Ser
1620 1625 1630

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Glu	Ala	Tyr	Asn	Asn	Val	Leu	Asp	Lys	Leu	Asn	Gly	Ile	Phe	Val	Val	
	1635						1640					1645				
Ile	Phe	Ser	Gly	Glu	Cys	Leu	Leu	Lys	Ile	Phe	Ala	Leu	Arg	Tyr	His	
	1650					1655					1660					
Tyr	Phe	Lys	Glu	Pro	Trp	Asn	Leu	Phe	Asp	Val	Val	Val	Val	Ile	Leu	
1665					1670					1675					1680	
Ser	Ile	Leu	Gly	Leu	Val	Leu	Ser	Asp	Ile	Ile	Glu	Lys	Tyr	Phe	Val	
				1685					1690					1695		
Ser	Pro	Thr	Leu	Leu	Arg	Val	Val	Arg	Val	Ala	Lys	Val	Gly	Arg	Val	
			1700					1705					1710			
Leu	Arg	Leu	Val	Lys	Gly	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	
	1715						1720					1725				
Leu	Ala	Met	Ser	Leu	Pro	Ala	Leu	Phe	Asn	Ile	Cys	Leu	Leu	Leu	Phe	
	1730					1735					1740					
Leu	Val	Met	Phe	Ile	Phe	Ala	Ile	Phe	Gly	Met	Ser	Phe	Phe	Met	His	
1745					1750					1755					1760	
Val	Lys	Glu	Lys	Ser	Gly	Ile	Asn	Ala	Val	Tyr	Asn	Phe	Lys	Thr	Phe	
				1765					1770					1775		
Gly	Gln	Ser	Met	Ile	Leu	Leu	Phe	Gln	Met	Ser	Thr	Ser	Ala	Gly	Trp	
			1780					1785					1790			
Asp	Gly	Val	Leu	Asp	Ala	Ile	Ile	Asn	Glu	Glu	Asp	Cys	Asp	Pro	Pro	
	1795						1800					1805				
Asp	Asn	Asp	Lys	Gly	Tyr	Pro	Gly	Asn	Cys	Gly	Ser	Ala	Thr	Val	Gly	
	1810					1815					1820					
Ile	Thr	Phe	Leu	Leu	Ser	Tyr	Leu	Val	Ile	Ser	Phe	Leu	Ile	Val	Ile	
1825					1830					1835					1840	
Asn	Met	Tyr	Ile	Ala	Val	Ile	Leu	Glu	Asn	Tyr	Ser	Gln	Ala	Thr	Glu	
				1845					1850					1855		
Asp	Val	Gln	Glu	Gly	Leu	Thr	Asp	Asp	Asp	Tyr	Asp	Met	Tyr	Tyr	Glu	
			1860					1865					1870			
Ile	Trp	Gln	Gln	Phe	Asp	Pro	Glu	Gly	Thr	Gln	Tyr	Ile	Arg	Tyr	Asp	
	1875						1880					1885				

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Gln Leu Ser Glu Phe Leu Asp Val Leu Glu Pro Pro Leu Gln Ile His
1890 1895 1900

Lys Pro Asn Lys Tyr Lys Ile Ile Ser Met Asp Met Pro Ile Cys Arg
1905 1910 1915 1920

Gly Asp Met Met Tyr Cys Val Asp Ile Leu Asp Ala Leu Thr Lys Asp
1925 1930 1935

Phe Phe Ala Arg Lys Gly Asn Pro Ile Glu Glu Thr Gly Glu Ile Gly
1940 1945 1950

Glu Ile Ala Ala Arg Pro Asp Thr Glu Gly Tyr Asp Pro Val Ser Ser
1955 1960 1965

Thr Leu Trp Arg Gln Arg Glu Glu Tyr Cys Ala Lys Leu Ile Gln Asn
1970 1975 1980

Ala Trp Arg Arg Tyr Lys Asn Gly Pro Pro Gln Glu Gly Asp Glu Gly
1985 1990 1995 2000

Glu Ala Ala Gly Gly Glu Asp Gly Ala Glu Gly Gly Glu Gly Glu Gly
2005 2010 2015

Gly Ser Gly Gly Gly Gly Gly Asp Asp Gly Gly Ser Ala Thr Gly Ala
2020 2025 2030

Thr Ala Ala Ala Gly Ala Thr Ser Pro Ser Asp Pro Asp Ala Gly Glu
2035 2040 2045

Ala Asp Gly Ala Ser Val Gly Gly Pro Leu Ser Pro Gly Cys Val Ser
2050 2055 2060

Gly Gly Ser Asn Gly Arg Gln Thr Ala Val Leu Val Glu Ser Asp Gly
2065 2070 2075 2080

Phe Val Thr Lys Asn Gly His Lys Val Val Ile His Ser Arg Ser Pro
2085 2090 2095

Ser Ile Thr Ser Arg Thr Ala Asp Val
2100 2105

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Glu	Asp	Ser	Asp	Ser	Ile	Ser	Glu	Glu	Glu	Arg	Ser	Leu	Phe	
1				5					10					15		
Arg	Pro	Phe	Thr	Arg	Glu	Ser	Leu	Leu	Gln	Ile	Glu	Gln	Arg	Ile	Ala	
			20					25					30			
Glu	His	Glu	Lys	Gln	Lys	Glu	Leu	Glu	Arg	Lys	Arg	Ala	Ala	Glu	Gly	
		35					40					45				
Glu	Gln	Ile	Arg	Tyr	Asp	Asp	Glu	Asp	Glu	Asp	Glu	Gly	Pro	Gln	Pro	
	50					55					60					
Asp	Pro	Thr	Leu	Glu	Gln	Gly	Val	Pro	Ile	Pro	Val	Arg	Met	Gln	Gly	
65					70					75					80	
Ser	Phe	Pro	Pro	Glu	Leu	Ala	Ser	Thr	Pro	Leu	Glu	Asp	Ile	Asp	Pro	
				85					90					95		
Phe	Tyr	Ser	Asn	Val	Leu	Thr	Phe	Val	Val	Ile	Ser	Lys	Gly	Lys	Asp	
			100					105					110			
Ile	Phe	Arg	Phe	Ser	Ala	Ser	Lys	Ala	Met	Trp	Leu	Leu	Asp	Pro	Phe	
		115					120					125				
Asn	Pro	Ile	Arg	Arg	Val	Ala	Ile	Tyr	Ile	Leu	Val	His	Pro	Leu	Phe	
	130					135					140					
Ser	Leu	Phe	Ile	Ile	Thr	Thr	Ile	Leu	Thr	Asn	Cys	Ile	Leu	Met	Ile	
145					150					155					160	
Met	Pro	Thr	Thr	Pro	Thr	Val	Glu	Ser	Thr	Glu	Val	Ile	Phe	Thr	Gly	
				165					170					175		
Ile	Tyr	Thr	Phe	Glu	Ser	Ala	Val	Lys	Val	Met	Ala	Arg	Gly	Phe	Ile	
			180					185					190			
Leu	Cys	Pro	Phe	Thr	Tyr	Leu	Arg	Asp	Ala	Trp	Asn	Trp	Leu	Asp	Phe	
		195					200					205				

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Val	Val	Ile	Ala	Leu	Ala	Tyr	Val	Thr	Met	Gly	Ile	Asp	Leu	Gly	Asn
	210					215					220				
Leu	Ala	Ala	Leu	Arg	Thr	Phe	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val
225					230					235					240
Ala	Ile	Val	Pro	Gly	Leu	Lys	Thr	Ile	Val	Gly	Ala	Val	Ile	Glu	Ser
				245					250					255	
Val	Lys	Asn	Leu	Arg	Asp	Val	Ile	Ile	Leu	Thr	Met	Phe	Ser	Leu	Ser
			260					265					270		
Val	Phe	Ala	Leu	Met	Gly	Leu	Gln	Ile	Tyr	Met	Gly	Val	Leu	Thr	Gln
		275					280					285			
Lys	Cys	Ile	Lys	Arg	Phe	Pro	Leu	Asp	Gly	Ser	Trp	Gly	Asn	Leu	Thr
	290					295					300				
Asp	Glu	Asn	Trp	Phe	Leu	His	Asn	Ser	Asn	Ser	Ser	Asn	Trp	Phe	Thr
305					310					315					320
Glu	Asn	Asp	Gly	Glu	Ser	Tyr	Pro	Val	Cys	Gly	Asn	Val	Ser	Gly	Ala
			325						330					335	
Gly	Gln	Cys	Gly	Glu	Asp	Tyr	Val	Cys	Leu	Gln	Gly	Phe	Gly	Pro	Asn
			340					345					350		
Pro	Asn	Tyr	Asp	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Gly	Trp	Ala	Phe	Leu
		355					360					365			
Ser	Ala	Phe	Arg	Leu	Met	Thr	Gln	Asp	Phe	Trp	Glu	Asp	Leu	Tyr	Gln
	370					375					380				
His	Val	Leu	Gln	Ala	Ala	Gly	Pro	Trp	His	Met	Leu	Phe	Phe	Ile	Val
385					390					395					400
Ile	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	Ile
				405					410					415	
Val	Ala	Met	Ser	Tyr	Asp	Glu	Leu	Gln	Lys	Lys	Ala	Glu	Glu	Glu	Glu
			420					425					430		
Ala	Ala	Glu	Glu	Glu	Ala	Ile	Arg	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Ala
		435					440					445			
Lys	Ala	Ala	Lys	Leu	Glu	Glu	Arg	Ala	Asn	Val	Ala	Ala	Gln	Ala	Ala
	450					455					460				

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Gln	Asp	Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ala	Leu	His	Pro	Glu	Met	Ala	
465					470					475					480	
Lys	Ser	Pro	Thr	Tyr	Ser	Cys	Ile	Ser	Tyr	Glu	Leu	Phe	Val	Gly	Gly	
				485					490					495		
Glu	Lys	Gly	Asn	Asp	Asp	Asn	Asn	Lys	Glu	Lys	Met	Ser	Ile	Arg	Ser	
			500					505					510			
Val	Glu	Val	Glu	Ser	Glu	Ser	Val	Ser	Val	Ile	Gln	Arg	Gln	Pro	Ala	
		515					520					525				
Pro	Thr	Thr	Ala	Pro	Ala	Thr	Lys	Val	Arg	Lys	Val	Ser	Thr	Thr	Ser	
	530					535					540					
Leu	Ser	Leu	Pro	Gly	Ser	Pro	Phe	Asn	Leu	Arg	Arg	Gly	Ser	Arg	Ser	
545					550					555					560	
Ser	His	Lys	Tyr	Thr	Ile	Arg	Asn	Gly	Arg	Gly	Arg	Phe	Gly	Ile	Pro	
				565					570					575		
Gly	Ser	Asp	Arg	Lys	Pro	Leu	Val	Leu	Gln	Thr	Tyr	Gln	Asp	Ala	Gln	
			580					585					590			
Gln	His	Leu	Pro	Tyr	Ala	Asp	Asp	Ser	Asn	Ala	Val	Thr	Pro	Met	Ser	
		595					600					605				
Glu	Glu	Asn	Gly	Ala	Ile	Ile	Val	Pro	Ala	Tyr	Tyr	Cys	Asn	Leu	Gly	
	610					615					620					
Ser	Arg	His	Ser	Ser	Tyr	Thr	Ser	His	Gln	Ser	Arg	Ile	Ser	Tyr	Thr	
625					630					635					640	
Ser	His	Gly	Asp	Leu	Leu	Gly	Gly	Met	Ala	Ala	Met	Gly	Ala	Ser	Thr	
				645					650					655		
Met	Thr	Lys	Glu	Ser	Lys	Leu	Arg	Ser	Arg	Asn	Thr	Arg	Asn	Gln	Ser	
			660					665								
Ile	Gly	Ala	Ala	Thr	Asn	Gly	Gly	Ser	Ser	Thr	Ala	Gly	Gly	Gly	Tyr	
		675					680					685				
Pro	Asp	Ala	Asn	His	Lys	Glu	Gln	Arg	Asp	Tyr	Glu	Met	Gly	Gln	Asp	
	690					695					700					
Tyr	Thr	Asp	Glu	Ala	Gly	Lys	Ile	Lys	His	His	Asp	Asn	Pro	Phe	Ile	
705					710					715					720	

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Glu	Pro	Val	Gln	Thr	Gln	Thr	Val	Val	Asp	Met	Lys	Asp	Val	Met	Val
				725					730					735	
Leu	Asn	Asp	Ile	Ile	Glu	Gln	Ala	Ala	Gly	Arg	His	Ser	Arg	Ala	Ser
			740					745					750		
Glu	Arg	Gly	Glu	Asp	Asp	Asp	Glu	Asp	Gly	Pro	Thr	Phe	Lys	Asp	Ile
		755					760					765			
Ala	Leu	Glu	Tyr	Ile	Leu	Lys	Gly	Ile	Glu	Ile	Phe	Cys	Val	Trp	Asp
	770					775					780				
Cys	Cys	Trp	Val	Trp	Leu	Lys	Phe	Gln	Glu	Trp	Val	Ser	Phe	Ile	Val
785					790					795					800
Phe	Asp	Pro	Phe	Val	Glu	Leu	Phe	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn
				805					810					815	
Thr	Met	Phe	Met	Ala	Met	Asp	His	His	Asp	Met	Asn	Pro	Glu	Leu	Glu
			820					825					830		
Lys	Val	Leu	Lys	Ser	Gly	Asn	Tyr	Phe	Phe	Thr	Ala	Thr	Phe	Ala	Ile
		835					840					845			
Glu	Ala	Ser	Met	Lys	Leu	Met	Ala	Met	Ser	Pro	Lys	Tyr	Tyr	Phe	Gln
	850					855					860				
Glu	Gly	Trp	Asn	Ile	Phe	Asp	Phe	Ile	Ile	Val	Ala	Leu	Ser	Leu	Leu
865					870					875					880
Glu	Leu	Gly	Leu	Glu	Gly	Val	Gln	Gly	Leu	Ser	Val	Leu	Arg	Ser	Phe
				885					890					895	
Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn
			900					905					910		
Leu	Leu	Ile	Ser	Ile	Met	Gly	Arg	Thr	Met	Gly	Ala	Leu	Gly	Asn	Leu
		915					920					925			
Thr	Phe	Val	Leu	Cys	Ile	Ile	Ile	Phe	Ile	Phe	Ala	Val	Met	Gly	Met
	930					935					940				
Gln	Leu	Phe	Gly	Lys	Asn	Tyr	Ile	Asp	His	Lys	Asp	Arg	Phe	Lys	Asp
945					950					955					960
His	Glu	Leu	Pro	Arg	Trp	Asn	Phe	Thr	Asp	Phe	Met	His	Ser	Phe	Met
				965					970					975	

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Ile	Val	Phe	Arg	Val	Leu	Cys	Gly	Glu	Trp	Ile	Glu	Ser	Met	Trp	Asp
			980					985					990		
Cys	Met	Tyr	Val	Gly	Asp	Val	Ser	Cys	Ile	Pro	Phe	Phe	Leu	Ala	Thr
		995					1000					1005			
Val	Val	Ile	Gly	Asn	Phe	Val	Val	Leu	Asn	Leu	Phe	Leu	Ala	Leu	Leu
	1010					1015					1020				
Leu	Ser	Asn	Phe	Gly	Ser	Ser	Ser	Leu	Ser	Ala	Pro	Thr	Ala	Asp	Asn
1025					1030					1035					1040
Asp	Thr	Asn	Lys	Ile	Ala	Glu	Ala	Phe	Asn	Arg	Ile	Ala	Arg	Phe	Lys
				1045					1050					1055	
Asn	Trp	Val	Lys	Arg	Asn	Ile	Ala	Asp	Cys	Phe	Lys	Leu	Ile	Arg	Asn
			1060					1065					1070		
Lys	Leu	Thr	Asn	Gln	Ile	Ser	Asp	Gln	Pro	Ser	Glu	His	Gly	Asp	Asn
		1075					1080					1085			
Glu	Leu	Glu	Leu	Gly	His	Asp	Glu	Ile	Met	Gly	Asp	Gly	Leu	Ile	Lys
	1090					1095					1100				
Lys	Gly	Met	Lys	Gly	Glu	Thr	Gln	Leu	Glu	Val	Ala	Ile	Gly	Asp	Gly
1105					1110					1115					1120
Met	Glu	Phe	Thr	Ile	His	Gly	Asp	Met	Lys	Asn	Asn	Lys	Pro	Lys	Lys
				1125					1130					1135	
Ser	Lys	Phe	Ile	Asn	Asn	Thr	Thr	Met	Ile	Gly	Asn	Ser	Ile	Asn	His
			1140					1145					1150		
Gln	Asp	Asn	Arg	Leu	Glu	His	Glu	Leu	Asn	His	Arg	Gly	Leu	Ser	Ile
		1155					1160					1165			
Gln	Asp	Asp	Asp	Thr	Ala	Ser	Ile	Asn	Ser	Tyr	Gly	Ser	His	Lys	Asn
	1170					1175					1180				
Arg	Pro	Phe	Lys	Asp	Glu	Ser	His	Lys	Gly	Ser	Ala	Glu	Thr	Ile	Glu
1185					1190					1195					1200
Gly	Glu	Glu	Lys	Arg	Asp	Val	Ser	Lys	Glu	Asp	Leu	Gly	Leu	Asp	Glu
				1205					1210					1215	
Glu	Leu	Asp	Glu	Glu	Ala	Glu	Gly	Asp	Glu	Gly	Gln	Leu	Asp	Gly	Asp
			1220					1225					1230		

Ile	Ile	Ile	His	Ala	Gln	Asn	Asp	Asp	Glu	Ile	Ile	Asp	Asp	Tyr	Pro	
			1235						1240					1245		
Ala	Asp	Cys	Phe	Pro	Asp	Ser	Tyr	Tyr	Lys	Lys	Phe	Pro	Ile	Leu	Ala	
			1250						1255					1260		
Gly	Asp	Glu	Asp	Ser	Pro	Phe	Trp	Gln	Gly	Trp	Gly	Asn	Leu	Arg	Leu	
			1265						1270					1275		
Lys	Thr	Phe	Gln	Leu	Ile	Glu	Asn	Lys	Tyr	Phe	Glu	Thr	Ala	Val	Ile	
									1285					1290		
Thr	Met	Ile	Leu	Met	Ser	Ser	Leu	Ala	Leu	Ala	Leu	Glu	Asp	Val	His	
									1300					1310		
Leu	Pro	Asp	Arg	Pro	Val	Met	Gln	Asp	Ile	Leu	Tyr	Tyr	Met	Asp	Arg	
									1315					1320		
Ile	Phe	Thr	Val	Ile	Phe	Phe	Leu	Glu	Met	Leu	Ile	Lys	Trp	Leu	Ala	
									1330					1335		
Leu	Gly	Phe	Lys	Val	Tyr	Phe	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp	Phe	
									1345					1350		
Val	Ile	Val	Met	Leu	Ser	Leu	Ile	Asn	Leu	Val	Ala	Val	Trp	Ser	Gly	
									1365					1370		
Leu	Asn	Asp	Ile	Ala	Val	Phe	Arg	Ser	Met	Arg	Thr	Leu	Arg	Ala	Leu	
									1380					1385		
Arg	Pro	Leu	Arg	Ala	Val	Ser	Arg	Trp	Glu	Gly	Met	Lys	Val	Val	Val	
									1395					1400		
Asn	Ala	Leu	Val	Gln	Ala	Ile	Pro	Ser	Ile	Phe	Asn	Val	Leu	Leu	Val	
									1410					1415		
Cys	Leu	Ile	Phe	Trp	Leu	Ile	Phe	Ala	Ile	Met	Gly	Val	Gln	Leu	Phe	
									1425					1430		
Ala	Gly	Lys	Tyr	Phe	Lys	Cys	Lys	Asp	Gly	Asn	Asp	Thr	Val	Leu	Ser	
									1445					1450		
His	Glu	Ile	Ile	Pro	Asn	Arg	Asn	Ala	Cys	Lys	Ser	Glu	Asn	Tyr	Thr	
									1460					1465		
Trp	Glu	Asn	Ser	Ala	Met	Asn	Phe	Asp	His	Val	Gly	Asn	Ala	Tyr	Leu	
									1475					1480		

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Cys	Leu	Phe	Gln	Val	Ala	Thr	Phe	Lys	Gly	Trp	Ile	Gln	Ile	Met	Asn		
1490						1495					1500						
Asp	Ala	Ile	Asp	Ser	Arg	Glu	Val	Asp	Lys	Gln	Pro	Ile	Arg	Glu	Thr		
1505					1510					1515					1520		
Asn	Ile	Tyr	Met	Tyr	Leu	Tyr	Phe	Val	Phe	Phe	Ile	Ile	Phe	Gly	Ser		
				1525					1530					1535			
Phe	Phe	Thr	Leu	Asn	Leu	Phe	Ile	Gly	Val	Ile	Ile	Asp	Asn	Phe	Asn		
			1540					1545					1550				
Glu	Gln	Lys	Lys	Lys	Ala	Gly	Gly	Ser	Leu	Glu	Met	Phe	Met	Thr	Glu		
		1555					1560					1565					
Asp	Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	Lys	Met	Gly	Ser	Lys	Lys		
1570						1575					1580						
Pro	Leu	Lys	Ala	Ile	Pro	Arg	Pro	Arg	Trp	Arg	Pro	Gln	Ala	Ile	Val		
1585					1590					1595					1600		
Phe	Glu	Ile	Val	Thr	Asp	Lys	Lys	Phe	Asp	Ile	Ile	Ile	Met	Leu	Phe		
				1605					1610					1615			
Ile	Gly	Leu	Asn	Met	Phe	Thr	Met	Thr	Leu	Asp	Arg	Tyr	Asp	Ala	Ser		
			1620					1625					1630				
Glu	Ala	Tyr	Asn	Asn	Val	Leu	Asp	Lys	Leu	Asn	Gly	Ile	Phe	Val	Val		
		1635					1640					1645					
Ile	Phe	Ser	Gly	Glu	Cys	Leu	Leu	Lys	Ile	Phe	Ala	Leu	Arg	Tyr	His		
	1650					1655					1660						
Tyr	Phe	Lys	Glu	Pro	Trp	Asn	Leu	Phe	Asp	Val	Val	Val	Val	Ile	Leu		
1665					1670					1675				1680			
Ser	Ile	Leu	Gly	Leu	Val	Leu	Ser	Asp	Ile	Ile	Glu	Lys	Tyr	Phe	Val		
			1685					1690						1695			
Ser	Pro	Thr	Leu	Leu	Arg	Val	Val	Arg	Val	Ala	Lys	Val	Gly	Arg	Val		
		1700						1705					1710				
Leu	Arg	Leu	Val	Lys	Gly	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala		
		1715					1720					1725					
Leu	Ala	Met	Ser	Leu	Pro	Ala	Leu	Phe	Asn	Ile	Cys	Leu	Leu	Leu	Phe		
	1730					1735					1740						

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Leu Val Met Phe Ile Phe Ala Ile Phe Gly Met Ser Phe Phe Met His	1745	1750	1755	1760
Val Lys Glu Lys Ser Gly Ile Asn Ala Val Tyr Asn Phe Lys Thr Phe	1765	1770	1775	
Gly Gln Ser Met Ile Leu Leu Phe Gln Met Ser Thr Ser Ala Gly Trp	1780	1785	1790	
Asp Gly Val Leu Asp Ala Ile Ile Asn Glu Glu Asp Cys Asp Pro Pro	1795	1800	1805	
Asp Asn Asp Lys Gly Tyr Pro Gly Asn Cys Gly Ser Ala Thr Val Gly	1810	1815	1820	
Ile Thr Phe Leu Leu Ser Tyr Leu Val Ile Ser Phe Leu Ile Val Ile	1825	1830	1835	1840
Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Tyr Ser Gln Ala Thr Glu	1845	1850	1855	
Asp Val Gln Glu Gly Leu Thr Asp Asp Asp Tyr Asp Met Tyr Tyr Glu	1860	1865	1870	
Ile Trp Gln Gln Phe Asp Pro Glu Gly Thr Gln Tyr Ile Arg Tyr Asp	1875	1880	1885	
Gln Leu Ser Glu Phe Leu Asp Val Leu Glu Pro Pro Leu Gln Ile His	1890	1895	1900	
Lys Pro Asn Lys Tyr Lys Ile Ile Ser Met Asp Met Pro Ile Cys Arg	1905	1910	1915	1920
Gly Asp Met Met Tyr Cys Val Asp Ile Leu Asp Ala Leu Thr Lys Asp	1925	1930	1935	
Phe Phe Ala Arg Lys Gly Asn Pro Ile Glu Glu Thr Gly Glu Ile Gly	1940	1945	1950	
Glu Ile Ala Ala Arg Pro Asp Thr Glu Gly Tyr Asp Pro Val Ser Ser	1955	1960	1965	
Thr Leu Trp Arg Gln Arg Glu Glu Tyr Cys Ala Lys Leu Ile Gln Asn	1970	1975	1980	
Ala Trp Arg Arg Tyr Lys Asn Gly Pro Pro Gln Glu Gly Asp Glu Gly	1985	1990	1995	2000

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Glu Ala Ala Gly Gly Glu Asp Gly Ala Glu Gly Gly Glu Gly Glu Gly
2005 2010 2015

Gly Ser Gly Gly Gly Gly Asp Asp Asp Gly Gly Ser Ala Thr Ala Ala
2020 2025 2030

Gly Ala Thr Ser Pro Thr Asp Pro Asp Ala Gly Glu Ala Asp Gly Ala
2035 2040 2045

Ser Ala Gly Asn Gly Gly Gly Pro Leu Ser Pro Gly Cys Val Ser Gly
2050 2055 2060

Gly Ser Asn Gly Arg Gln Thr Ala Val Leu Val Glu Ser Asp Gly Phe
2065 2070 2075 2080

Val Thr Lys Asn Gly His Lys Val Val Ile His Ser Arg Ser Pro Ser
2085 2090 2095

Ile Thr Ser Arg Thr Ala Asp Val
2100

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGTTGGGCT TTCCTGTC

18

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

09428374.102899
668207.1282460

GGGAATTCRA ADATRTTCCA NCCYTC

26

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGARGAYA THGAYCYNTA YTA

23

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGTATCGCCT CCTCCTCG

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCTAGAT HTTYGCNATH TTYGGNATG

29

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGAATTCN GGRTCRAAYT GYTGCCA

27

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGTCTAGAR GANCARAARA ARTAYTA

27

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCATACTTTG GCCCAATGTC

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCCGAATTAG AGAAGGTGCT G

21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTATTGCTT GTGGTCGCCA C

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATCNTTRGC NGCNTAGACN ATGAC

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATTGAATGG ATCGAGCAGC C

21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGTTTCTCCT TTCATATCTA G

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGBGBBGG NCKBGGNCKN GCTCA

25

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Thr	Glu	Asp	Ser	Asp	Ser	Ile	Ser	Glu	Glu	Glu	Arg	Ser	Leu	Phe
1				5					10					15	
Arg	Pro	Phe	Thr	Arg	Glu	Ser	Leu	Val	Gln	Ile	Glu	Gln	Arg	Ile	Ala
			20					25					30		
Ala	Glu	His	Glu	Lys	Gln	Lys	Glu	Leu	Glu	Arg	Lys	Arg	Ala	Glu	Gly
		35					40					45			
Glu	Val	Pro	Arg	Tyr	Gly	Arg	Lys	Lys	Lys	Gln	Lys	Glu	Ile	Arg	Tyr
	50					55					60				
Asp	Asp	Glu	Asp	Glu	Asp	Glu	Gly	Pro	Gln	Pro	Asp	Pro	Thr	Leu	Glu
65					70					75					80
Gln	Gly	Val	Pro	Ile	Pro	Val	Arg	Leu	Gln	Gly	Ser	Phe	Pro	Pro	Glu
				85					90					95	
Leu	Ala	Ser	Thr	Pro	Leu	Glu	Asp	Ile	Asp	Pro	Tyr	Tyr	Ser	Asn	Val
			100					105					110		
Leu	Thr	Phe	Val	Val	Val	Ser	Lys	Gly	Lys	Asp	Ile	Phe	Arg	Phe	Ser
		115					120					125			
Ala	Ser	Lys	Ala	Met	Trp	Met	Leu	Asp	Pro	Phe	Asn	Pro	Ile	Arg	Arg
	130					135					140				
Val	Ala	Ile	Tyr	Ile	Leu	Val	His	Pro	Leu	Phe	Ser	Leu	Phe	Ile	Ile
145					150					155					160
Thr	Thr	Ile	Leu	Val	Asn	Cys	Ile	Leu	Met	Ile	Met	Pro	Thr	Thr	Pro
			165						170					175	
Thr	Val	Glu	Ser	Thr	Glu	Val	Ile	Phe	Thr	Gly	Ile	Tyr	Thr	Phe	Glu
			180					185					190		
Ser	Ala	Val	Lys	Val	Met	Ala	Arg	Gly	Phe	Ile	Leu	Cys	Pro	Phe	Thr
		195					200					205			
Tyr	Leu	Arg	Asp	Ala	Trp	Asn	Trp	Leu	Asp	Phe	Val	Val	Ile	Ala	Leu
	210					215					220				
Ala	Tyr	Val	Thr	Met	Gly	Ile	Asp	Leu	Gly	Asn	Leu	Ala	Ala	Leu	Arg
225					230					235					240

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Thr	Phe	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ala	Ile	Val	Pro	Gly	
				245					250					255		
Leu	Lys	Thr	Ile	Val	Gly	Ala	Val	Ile	Glu	Ser	Val	Lys	Asn	Leu	Arg	
			260					265					270			
Asp	Val	Ile	Ile	Leu	Thr	Met	Phe	Ser	Leu	Ser	Val	Phe	Ala	Leu	Met	
		275					280					285				
Gly	Leu	Gln	Ile	Tyr	Met	Gly	Val	Leu	Thr	Glu	Lys	Cys	Ile	Lys	Lys	
	290					295					300					
Phe	Pro	Leu	Asp	Gly	Ser	Trp	Gly	Asn	Leu	Thr	Asp	Glu	Asn	Trp	Asp	
305					310					315					320	
Tyr	His	Asn	Arg	Asn	Ser	Ser	Asn	Trp	Tyr	Ser	Glu	Asp	Glu	Gly	Ile	
				325					330					335		
Ser	Phe	Pro	Leu	Cys	Gly	Asn	Ile	Ser	Gly	Ala	Gly	Gln	Cys	Asp	Asp	
			340					345					350			
Asp	Tyr	Val	Cys	Leu	Gln	Gly	Phe	Gly	Pro	Asn	Pro	Asn	Tyr	Gly	Tyr	
		355					360					365				
Thr	Ser	Phe	Asp	Ser	Phe	Gly	Trp	Ala	Phe	Leu	Ser	Ala	Phe	Arg	Leu	
	370					375					380					
Met	Thr	Gln	Asp	Phe	Trp	Glu	Asp	Leu	Tyr	Gln	Leu	Val	Leu	Arg	Ala	
385					390					395					400	
Ala	Gly	Pro	Trp	His	Met	Leu	Phe	Phe	Ile	Val	Ile	Ile	Phe	Leu	Gly	
				405					410					415		
Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	Ile	Val	Ala	Met	Ser	Tyr	
			420					425					430			
Asp	Glu	Leu	Gln	Arg	Lys	Ala	Glu	Glu	Glu	Glu	Ala	Ala	Glu	Glu	Glu	
		435					440					445				
Ala	Ile	Arg	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Ala	Lys	Ala	Ala	Lys	Leu	
						455					460					
Glu	Glu	Arg	Ala	Asn	Ala	Gln	Ala	Gln	Ala	Ala	Ala	Asp	Ala	Ala	Ala	
465					470				475						480	
Ala	Glu	Glu	Ala	Ala	Leu	His	Pro	Glu	Met	Ala	Lys	Ser	Pro	Thr	Tyr	

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485										490					495				
Ser	Cys	Ile	Ser	Tyr	Glu	Leu	Phe	Val	Gly	Gly	Glu	Lys	Gly	Asn	Asp				
			500					505					510						
Asp	Asn	Asn	Lys	Glu	Lys	Met	Ser	Ile	Arg	Ser	Val	Glu	Val	Glu	Ser				
		515					520					525							
Glu	Ser	Val	Ser	Val	Ile	Gln	Arg	Gln	Pro	Ala	Pro	Thr	Thr	Ala	His				
	530					535					540								
Gln	Ala	Thr	Lys	Val	Arg	Lys	Val	Ser	Thr	Thr	Ser	Leu	Ser	Leu	Pro				
545					550					555					560				
Gly	Ser	Pro	Phe	Asn	Ile	Arg	Arg	Gly	Ser	Arg	Ser	Ser	His	Lys	Tyr				
				565					570					575					
Thr	Ile	Arg	Asn	Gly	Arg	Gly	Arg	Phe	Gly	Ile	Pro	Gly	Ser	Asp	Arg				
			580					585					590						
Lys	Pro	Leu	Val	Leu	Ser	Thr	Tyr	Gln	Asp	Ala	Gln	Gln	His	Leu	Pro				
		595					600					605							
Tyr	Ala	Asp	Asp	Ser	Asn	Ala	Val	Thr	Pro	Met	Ser	Glu	Glu	Asn	Gly				
	610					615					620								
Ala	Ile	Ile	Val	Pro	Val	Tyr	Tyr	Gly	Asn	Leu	Gly	Ser	Arg	His	Ser				
625					630					635					640				
Ser	Tyr	Thr	Ser	His	Gln	Ser	Arg	Ile	Ser	Tyr	Thr	Ser	His	Gly	Asp				
				645					650					655					
Leu	Leu	Gly	Gly	Met	Ala	Val	Met	Gly	Val	Ser	Thr	Met	Thr	Lys	Glu				
			660					665					670						
Ser	Lys	Leu	Arg	Asn	Arg	Asn	Thr	Arg	Asn	Gln	Ser	Val	Gly	Ala	Thr				
		675					680					685							
Asn	Gly	Gly	Thr	Thr	Cys	Leu	Asp	Thr	Asn	His	Lys	Leu	Asp	His	Arg				
	690					695					700								
Asp	Tyr	Glu	Ile	Gly	Leu	Glu	Cys	Thr	Asp	Glu	Ala	Gly	Lys	Ile	Lys				
705					710					715					720				
His	His	Asp	Asn	Pro	Phe	Ile	Glu	Pro	Val	Gln	Thr	Gln	Thr	Val	Val				
				725					730					735					

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Asp	Met	Lys	Asp	Val	Met	Val	Leu	Asn	Asp	Ile	Ile	Glu	Gln	Ala	Ala		
			740					745					750				
Gly	Arg	His	Ser	Arg	Ala	Ser	Asp	Arg	Gly	Glu	Asp	Asp	Asp	Glu	Asp		
		755					760					765					
Gly	Pro	Thr	Phe	Lys	Asp	Lys	Ala	Leu	Glu	Val	Ile	Leu	Lys	Gly	Ile		
	770					775					780						
Asp	Val	Phe	Cys	Val	Trp	Asp	Cys	Cys	Trp	Val	Trp	Leu	Lys	Phe	Gln		
785					790					795					800		
Glu	Trp	Val	Ser	Leu	Ile	Val	Phe	Asp	Pro	Phe	Val	Glu	Leu	Phe	Ile		
			805						810					815			
Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Met	Phe	Met	Ala	Met	Asp	His	His		
		820						825					830				
Asp	Met	Asn	Lys	Glu	Met	Glu	Arg	Val	Leu	Lys	Ser	Gly	Asn	Tyr	Phe		
		835					840					845					
Phe	Thr	Ala	Thr	Phe	Ala	Ile	Glu	Ala	Thr	Met	Lys	Leu	Met	Ala	Met		
	850					855					860						
Ser	Pro	Lys	Tyr	Tyr	Phe	Gln	Glu	Gly	Trp	Asn	Ile	Phe	Asp	Phe	Ile		
865					870					875					880		
Ile	Val	Ala	Leu	Ser	Leu	Leu	Glu	Leu	Gly	Leu	Glu	Gly	Val	Gln	Gly		
			885						890					895			
Leu	Ser	Val	Leu	Arg	Ser	Phe	Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala		
			900					905					910				
Lys	Ser	Trp	Pro	Thr	Leu	Asn	Leu	Leu	Ile	Ser	Ile	Met	Gly	Arg	Thr		
		915					920					925					
Met	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Phe	Val	Leu	Cys	Ile	Ile	Ile	Phe		
	930					935					940						
Ile	Phe	Ala	Val	Met	Gly	Met	Gln	Leu	Phe	Gly	Lys	Asn	Tyr	His	Asp		
945					950					955					960		
His	Lys	Asp	Arg	Phe	Pro	Asp	Gly	Asp	Leu	Pro	Arg	Trp	Asn	Phe	Thr		
				965					970					975			
Asp	Phe	Met	His	Ser	Phe	Met	Ile	Val	Phe	Arg	Val	Leu	Cys	Gly	Glu		
			980					985					990				

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Trp Ile Glu Ser Met Trp Asp Cys Met Tyr Val Gly Asp Val Ser Cys
995 1000 1005

Ile Pro Phe Phe Leu Ala Thr Val Val Ile Gly Asn Leu Val Val Leu
1010 1015 1020

Asn Leu Phe Leu Ala Leu Leu Leu Ser Asn Phe Gly Ser Ser Ser Leu
1025 1030 1035 1040

Ser Ala Pro Thr Ala Asp Asn Asp Thr Asn Lys Ile Ala Glu Ala Phe
1045 1050 1055

Asn Arg Ile Gly Arg Phe Lys Ser Trp Val Lys Arg Asn Ile Ala Asp
1060 1065 1070

Cys Phe Lys Leu Ile Arg Asn Lys Leu Thr Asn Gln Ile Ser Asp Gln
1075 1080 1085

Pro Ser Glu His Gly Asp Asn Glu Leu Glu Leu Gly His Asp Glu Ile
1090 1095 1100

Leu Ala Asp Gly Leu Ile Lys Lys Gly Ile Lys Glu Gln Thr Gln Leu
1105 1110 1115 1120

Glu Val Ala Ile Gly Asp Gly Met Glu Phe Thr Ile His Gly Asp Met
1125 1130 1135

Lys Asn Asn Lys Pro Lys Lys Ser Lys Tyr Leu Asn Asn Ala Thr Asp
1140 1145 1150

Asp Asp Thr Ala Ser Ile Asn Ser Tyr Gly Ser His Lys Asn Arg Pro
1155 1160 1165

Phe Lys Asp Glu Ser His Lys Gly Ser Ala Glu Thr Met Glu Gly Glu
1170 1175 1180

Glu Lys Arg Asp Ala Ser Lys Glu Asp Leu Gly Leu Asp Glu Glu Leu
1185 1190 1195 1200

Asp Glu Glu Gly Glu Cys Glu Glu Gly Pro Leu Asp Gly Asp Ile Ile
1205 1210 1215

Ile His Ala His Asp Glu Asp Ile Leu Asp Glu Tyr Pro Ala Asp Cys
1220 1225 1230

Cys Pro Asp Ser Tyr Tyr Lys Lys Phe Pro Ile Leu Ala Gly Asp Asp
1235 1240 1245

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Asp	Ser	Pro	Phe	Trp	Gln	Gly	Trp	Gly	Asn	Leu	Arg	Leu	Lys	Thr	Phe	
1250						1255						1260				
Arg	Leu	Ile	Glu	Asp	Lys	Tyr	Phe	Glu	Thr	Ala	Val	Ile	Thr	Met	Ile	
1265					1270					1275					1280	
Leu	Met	Ser	Ser	Leu	Ala	Leu	Ala	Leu	Glu	Asp	Val	His	Leu	Pro	Gln	
				1285					1290					1295		
Arg	Pro	Ile	Leu	Gln	Asp	Ile	Leu	Tyr	Tyr	Met	Asp	Arg	Ile	Phe	Thr	
			1300					1305					1310			
Val	Ile	Phe	Phe	Leu	Glu	Met	Leu	Ile	Lys	Trp	Leu	Ala	Leu	Gly	Phe	
		1315					1320					1325				
Lys	Val	Tyr	Leu	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp	Phe	Val	Ile	Val	
1330						1335					1340					
Met	Val	Ser	Leu	Ile	Asn	Phe	Val	Ala	Ser	Leu	Val	Gly	Ala	Gly	Gly	
1345					1350					1355					1360	
Ile	Gln	Ala	Phe	Lys	Thr	Met	Arg	Thr	Leu	Arg	Ala	Leu	Arg	Pro	Leu	
				1365					1370					1375		
Arg	Ala	Met	Ser	Arg	Met	Gln	Gly	Met	Arg	Val	Val	Val	Asn	Ala	Leu	
			1380					1385					1390			
Val	Gln	Ala	Ile	Pro	Ser	Ile	Phe	Asn	Val	Leu	Leu	Val	Cys	Leu	Ile	
		1395					1400					1405				
Phe	Trp	Leu	Ile	Phe	Ala	Ile	Met	Gly	Val	Gln	Leu	Phe	Ala	Gly	Lys	
	1410					1415					1420					
Tyr	Phe	Lys	Cys	Glu	Asp	Met	Asn	Gly	Thr	Lys	Leu	Ser	His	Glu	Ile	
1425					1430					1435					1440	
Ile	Pro	Asn	Arg	Asn	Ala	Cys	Glu	Ser	Glu	Asn	Tyr	Thr	Trp	Val	Asn	
				1445					1450					1455		
Ser	Ala	Met	Asn	Phe	Asp	His	Val	Gly	Asn	Ala	Tyr	Leu	Cys	Leu	Phe	
			1460					1465					1470			
Gln	Val	Ala	Thr	Phe	Lys	Gly	Trp	Ile	Gln	Ile	Met	Asn	Asp	Ala	Ile	
		1475					1480					1485				
Asp	Ser	Arg	Glu	Val	Asp	Lys	Gln	Pro	Ile	Arg	Glu	Thr	Asn	Ile	Tyr	
1490						1495					1500					

Met Tyr Leu Tyr Phe Val Phe Phe Ile Ile Phe Gly Ser Phe Phe Thr
1505 1510 1515 1520

Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Glu Gln Lys
1525 1530 1535

Lys Lys Ala Gly Gly Ser Leu Glu Met Phe Met Thr Glu Asp Gln Lys
1540 1545 1550

Lys Tyr Tyr Ser Ala Met Lys Lys Met Gly Ser Lys Lys Pro Leu Lys
1555 1560 1565

Ala Ile Pro Arg Pro Arg Trp Arg Pro Gln Ala Ile Val Phe Glu Ile
1570 1575 1580

Val Thr Asp Lys Lys Phe Asp Ile Ile Ile Met Leu Phe Ile Gly Leu
1585 1590 1595 1600

Asn Met Phe Thr Met Thr Leu Asp Arg Tyr Asp Ala Ser Asp Thr Tyr
1605 1610 1615

Asn Ala Val Leu Asp Tyr Leu Asn Ala Ile Phe Val Val Ile Phe Ser
1620 1625 1630

Ser Glu Cys Leu Leu Lys Ile Phe Ala Leu Arg Tyr His Tyr Phe Ile
1635 1640 1645

Glu Pro Trp Asn Leu Phe Asp Val Val Val Val Ile Leu Ser Ile Leu
1650 1655 1660

Gly Leu Val Leu Ser Asp Ile Ile Glu Lys Tyr Phe Val Ser Pro Thr
1665 1670 1675 1680

Leu Leu Arg Val Val Arg Val Ala Lys Val Gly Arg Val Leu Arg Leu
1685 1690 1695

Val Lys Gly Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu Ala Met
1700 1705 1710

Ser Leu Pro Ala Leu Phe Asn Ile Cys Leu Leu Leu Phe Leu Val Met
1715 1720 1725

Phe Ile Phe Ala Ile Phe Gly Met Ser Phe Phe Met His Val Lys Glu
1730 1735 1740

Lys Ser Gly Ile Asn Asp Val Tyr Asn Phe Lys Thr Phe Gly Gln Ser
1745 1750 1755 1760

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Met Ile Leu Leu Phe Gln Met Ser Thr Ser Ala Gly Trp Asp Gly Val
1765 1770 1775

Leu Asp Ala Ile Ile Asn Glu Glu Ala Cys Asp Pro Pro Asp Asn Asp
1780 1785 1790

Lys Gly Tyr Pro Gly Asn Cys Gly Ser Ala Thr Val Gly Ile Thr Phe
1795 1800 1805

Leu Leu Ser Tyr Leu Val Ile Ser Phe Leu Ile Val Ile Asn Met Tyr
1810 1815 1820

Ile Ala Val Ile Leu Glu Asn Tyr Ser Gln Ala Thr Glu Asp Val Gln
1825 1830 1835 1840

Glu Gly Leu Thr Asp Asp Asp Tyr Asp Met Tyr Tyr Glu Ile Trp Gln
1845 1850 1855

Gln Phe Asp Pro Glu Gly Thr Gln Tyr Ile Arg Tyr Asp Gln Leu Ser
1860 1865 1870

Glu Phe Leu Asp Val Leu Glu Pro Pro Leu Gln Ile His Lys Pro Asn
1875 1880 1885

Lys Tyr Lys Ile Ile Ser Met Asp Ile Pro Ile Cys Arg Gly Asp Leu
1890 1895 1900

Met Tyr Cys Val Asp Ile Leu Asp Ala Leu Thr Lys Asp Phe Phe Ala
1905 1910 1915 1920

Arg Lys Gly Asn Pro Ile Glu Glu Thr Gly Glu Ile Gly Glu Ile Ala
1925 1930 1935

Ala Arg Pro Asp Thr Glu Gly Tyr Glu Pro Val Ser Ser Thr Leu Trp
1940 1945 1950

Arg Gln Arg Glu Glu Tyr Cys Ala Arg Leu Ile Gln His Ala Trp Arg
1955 1960 1965

Lys His Lys Ala Arg Gly Glu Gly Gly Gly Ser Phe Glu Pro Asp Thr
1970 1975 1980

Asp His Gly Asp Gly Gly Asp Pro Asp Ala Gly Asp Pro Ala Pro Asp
1985 1990 1995 2000

Glu Ala Thr Asp Gly Asp Ala Pro Ala Gly Gly Asp Gly Ser Val Asn
2005 2010 2015

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Gly Thr Ala Glu Gly Ala Ala Asp Ala Asp Glu Ser Asn Val Asn Ser
2020 2025 2030

Pro Gly Glu Asp Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
2035 2040 2045

Ala Ala Gly Thr Thr Thr Ala Gly Ser Pro Gly Ala Gly Ser Ala Gly
2050 2055 2060

Arg Gln Thr Ala Val Leu Val Glu Ser Asp Gly Phe Val Thr Lys Asn
2065 2070 2075 2080

Gly His Lys Val Val Ile His Ser Arg Ser Pro Ser Ile Thr Ser Arg
2085 2090 2095

Thr Ala Asp Val
2100

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